Sequence Range: 1 to 494

5' primer region

```
        10          20          30              40          50
 *       *     *          *        *        *       *        *
TTACKRGWMK WC ATG RRA TGS ASC TRK RTC ATY YTC TTC TTG GTA TCA ACA
              M   X   X   X   X   X   I   X   F   L   V   S   T>
```

```
        60          70          80      FW L    90
 *       *     *     *         *        *        *        *
GCT ACA AGT GTC CAC TCC CAG GTC CAA CTG CAG CAG CCT GGG GCT GAG
 A   T   S   V   H   S   Q   V   Q   L   Q   Q   P   G   A   E>
```

signal peptide cleavage site

```
100         110                 120         130         140
 *       *        *         *        *        *        *
CTT GTG AAG CCT GGG ACT TCA GTG AAG CTG TCC TGC AAG GGT TAT GGC
 L   V   K   P   G   T   S   V   K   L   S   C   K   G   Y   G>
```

```
150                 160      CDR1 170        180   FW 2   190
 *              *        *        *        *        *        *
TAC ACC TTC ACC AGC TAC TGG ATG CAC TGG GTG AAG CAG AGG CCT GGA
 Y   T   F   T   S   Y   W   M   H   W   V   K   Q   R   P   G>
```

```
200             210             220   CDR2  230         240
 *          *        *        *        *        *        *
CAA GGC CTT GAG TGG ATC GGA GAG ATT GAT CCT TCT GAG AGT AAT ACT
 Q   G   L   E   W   I   G   E   I   D   P   S   E   S   N   T>
```

```
        250         260             270   FW3  280         290
 *          *        *        *        *        *        *
AAC TAC AAT CAA AAA TTC AAG GGC AAG GCC ACA TTG ACT GTA GAC ATT
 N   Y   N   Q   K   F   K   G   K   A   T   L   T   V   D   I>
```

```
        300         310         320         330
 *          *        *        *        *        *
TCC TCC AGC ACA GCC TAC ATG CAG CTC AGC AGC CTG ACA TCT GAG GAC
 S   S   S   T   A   Y   M   Q   L   S   S   L   T   S   E   D>
```

```
340         350   FW3     360             370 CDR3  380
 *          *        *        *        *        *        *
TCT GCG GTC TAC TAT TGT GCA AGA GGG GGT TAC GAC GGA TGG GAC TAT
 S   A   V   Y   Y   C   A   R   G   G   Y   D   G   W   D   Y>
```

```
        400   FW4  410         420         430      C H
390         *        *        *        *        *
GCT ATT GAC TAC TGG GGT CAA GGC ACC TCA GTC ACC GTC TCC TCA GCC
 A   I   D   Y   W   G   Q   G   T   S   V   T   V   S   S   A>
```

```
        440         450         460         470         480         490
 *          *        *        *        *        *        *        *
AAA ACG ACA CCRYCN CSYKTMTMYC YYSBDNNCCC YKGRWSCYTG GNNGAAGCTT
 K   T   T>
```

3' primer region

GGGA

FIGURE 1

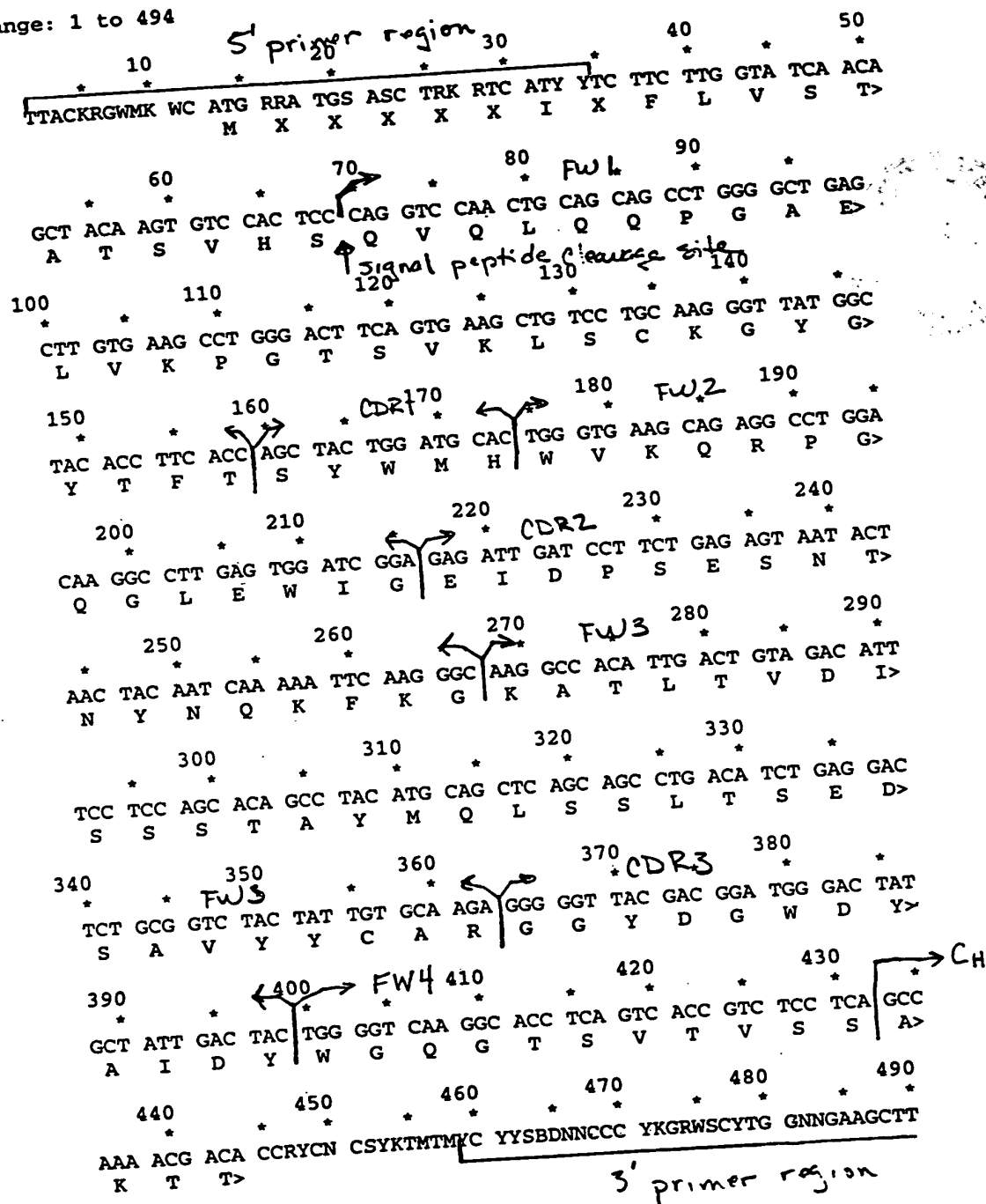Sequence Range: 1 to 428

```
                    10            20              30            40              50
                     *             *               *             *               *
         *         *         *            *              *             *
     TTACTTGACG ACTCGGG ATG GGA TGG AGC TAT ATC ATC TTC TTC TTG GTA TCA
                         M   G   W   S   Y   I   I   F   F   L   V   S>

            60              70              80              90             100
             *               *               *               *               *
        *         *             *               *             *
     ACA GCT ACA AGT GTC CAC TCC CAG GTC CAA CTG CAG CAG CCT GGG GCT
      T   A   T   S   V   H   S   Q   V   Q   L   Q   Q   P   G   A>

              110            120           130             140
               *             *             *               *             *
          *         *             *             *
     GAG CTT GTG AAG CCT GGG ACT TCA GTG AAG CTG TCC TGC AAG GGT TAT
      E   L   V   K   P   G   T   S   V   K   L   S   C   K   G   Y>

     150           160             170           180            190
      *             *               *             *              *             *
                                         *             *
     GGC TAC ACC TTC ACC AGC TAC TGG ATG CAC TGG GTG AAG CAG AGG CCT
      G   Y   T   F   T   S   Y   W   M   H   W   V   K   Q   R   P>

                          210             220           230             240
     200                   *               *             *               *
      *             *             *             *             *             *
     GGA CAA GGC CTT GAG TGG ATC GGA GAG ATT GAT CCT TCT GAG AGT AAT
      G   Q   G   L   E   W   I   G   E   I   D   P   S   E   S   N>

              250             260           270             280             290
               *               *             *               *               *
                    *             *             *             *
     ACT AAC TAC AAT CAA AAA TTC AAG GGC AAG GCC ACA TTG ACT GTA GAC
      T   N   Y   N   Q   K   F   K   G   K   A   T   L   T   V   D>

                        300             310           320             330             340
                         *               *             *             *             *
          *             *             *             *
     ATT TCC TCC AGC ACA GCC TAC ATG CAG CTC AGC AGC CTG ACA TCT GAG
      I   S   S   S   T   A   Y   M   Q   L   S   S   L   T   S   E>

                        350             360           370             380
                         *               *             *             *             *
               *             *             *             *
     GAC TCT GCG GTC TAC TAT TGT GCA AGA GGG GGT TAC GAC GGA TGG GAC
      D   S   A   V   Y   Y   C   A   R   G   G   Y   D   G   W   D>

              400             410           420
               *               *             *             *
     390                   *
      *             *
     TAT GCT ATT GAC TAC TGG GGT CAA GGC ACA TCA GTC ACC
      Y   A   I   D   Y   W   G   Q   G   T   S   V   T>
```
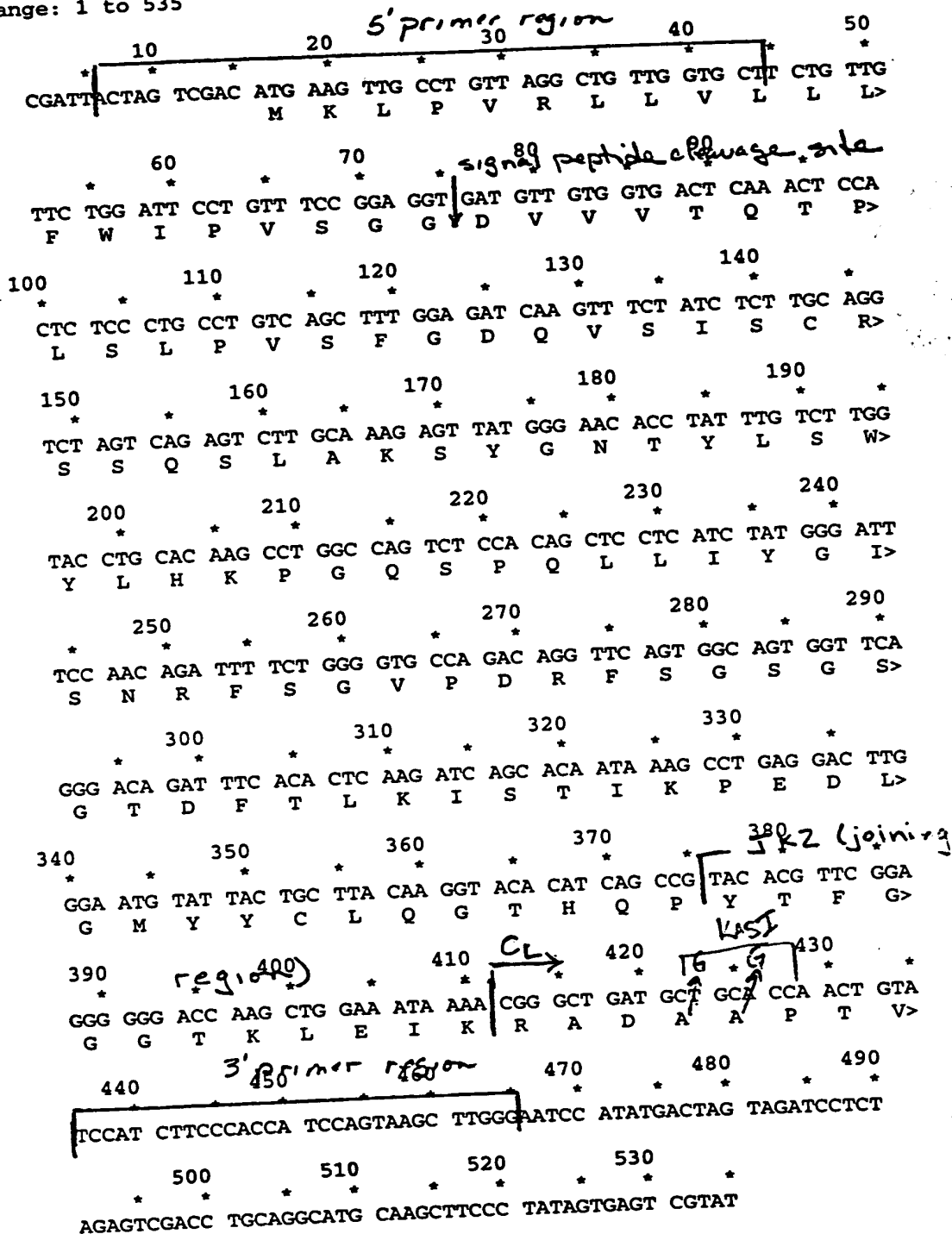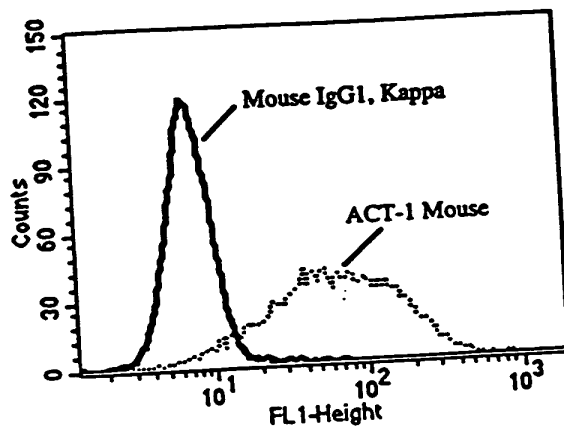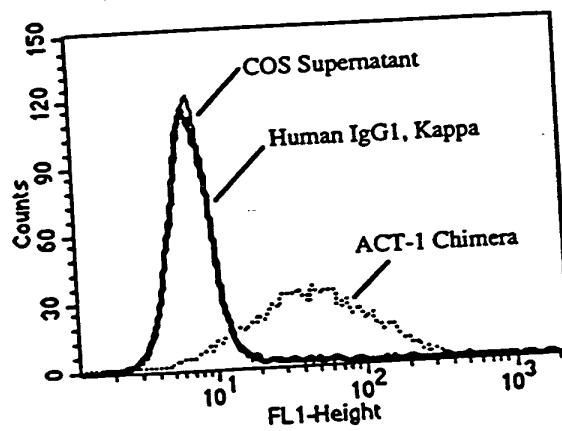
FIGURE 2

Sequence Range: 1 to 535

5' primer region

signal peptide cleavage site

JK2 (joining

region)

CL>

VASI

3' primer region

```
       10            20        30            40            50
        *       *    *     *     *      *      *     *     *
  CGATTACTAG TCGAC ATG AAG TTG CCT GTT AGG CTG TTG GTG CTT CTG TTG
                    M   K   L   P   V   R   L   L   V   L   L   L>

       60            70        80            90
        *       *    *     *     *      *      *     *     *
  TTC TGG ATT CCT GTT TCC GGA GGT GAT GTT GTG GTG ACT CAA ACT CCA
   F   W   I   P   V   S   G   G   D   V   V   V   T   Q   T   P>

100          110       120        130          140
 *       *    *     *    *      *     *     *      *     *
CTC TCC CTG CCT GTC AGC TTT GGA GAT CAA GTT TCT ATC TCT TGC AGG
 L   S   L   P   V   S   F   G   D   Q   V   S   I   S   C   R>

150          160       170        180          190
 *       *    *     *    *      *     *     *      *     *     *
TCT AGT CAG AGT CTT GCA AAG AGT TAT GGG AAC ACC TAT TTG TCT TGG
 S   S   Q   S   L   A   K   S   Y   G   N   T   Y   L   S   W>

200          210       220        230          240
 *       *    *     *    *      *     *     *      *     *
TAC CTG CAC AAG CCT GGC CAG TCT CCA CAG CTC CTC ATC TAT GGG ATT
 Y   L   H   K   P   G   Q   S   P   Q   L   L   I   Y   G   I>

       250       260        270          280          290
 *       *    *     *    *      *     *     *      *     *     *
TCC AAC AGA TTT TCT GGG GTG CCA GAC AGG TTC AGT GGC AGT GGT TCA
 S   N   R   F   S   G   V   P   D   R   F   S   G   S   G   S>

          300       310        320          330
 *       *    *     *    *      *     *     *      *     *
GGG ACA GAT TTC ACA CTC AAG ATC AGC ACA ATA AAG CCT GAG GAC TTG
 G   T   D   F   T   L   K   I   S   T   I   K   P   E   D   L>

340          350       360        370          380
 *       *    *     *    *      *     *     *      *
GGA ATG TAT TAC TGC TTA CAA GGT ACA CAT CAG CCG TAC ACG TTC GGA
 G   M   Y   Y   C   L   Q   G   T   H   Q   P   Y   T   F   G>

390          400       410        420          430
 *       *    *     *    *      *     *     *      *     *
GGG GGG ACC AAG CTG GAA ATA AAA CGG GCT GAT GCT GCA CCA ACT GTA
 G   G   T   K   L   E   I   K   R   A   D   A   A   P   T   V>

       440       450       460        470          480          490
 *       *    *     *    *      *      *     *      *     *     *
TCCAT CTTCCCACCA TCCAGTAAGC TTGGGAATCC ATATGACTAG TAGATCCTCT

          500       510        520          530
 *       *    *     *    *      *     *      *
AGAGTCGACC TGCAGGCATG CAAGCTTCCC TATAGTGAGT CGTAT
```

FIGURE 3

FIGURE 4A

FIGURE 4B

Percent Identity: 71.429

Percent Similarity: 82.143

```
Act-1.vl    1 DVVVTQTPLSLPVSFGDQVSISC[RSSQSLAKSYGNTYLS]WYLHKPGQSPQ  50
              ||| : | ||||||| : : : ||||||||  :: ::  :  ||| ||||||
GM607'CL    1 DIVMTQSPLSLPVTPGEPASISC[RSSQSLLHSNGYNYLD]WYLQKPGQSPQ  50
                                      [     CDR 1        ]
```

```
Act-1.vl   51 LLIY[GISNRFS]GVPDRFSGSGSGTDFTLKISTIKPEDLGHYYC[LQGTHQP 100
              |||| | | || |||||||||||||||||||| : : :: : :  : : :  |
GM607'CL   51 LLIY[LGSNRAS]GVPDRFSGSGSGTDFTLKISRVEAEDVGVYYC[MQALQTP 100
                  [ CDR 2 ]                               [ CDR 3
```

```
Act-1.vl  101 YT]FGGGTKLEIK 112
              ||  || : ||| :|
GM607'CL  101 QT]FGQGTKVEIK 112
              ]
```

FIGURE 5

Percent Similarity: 82.353

Percent Identity: 68.067
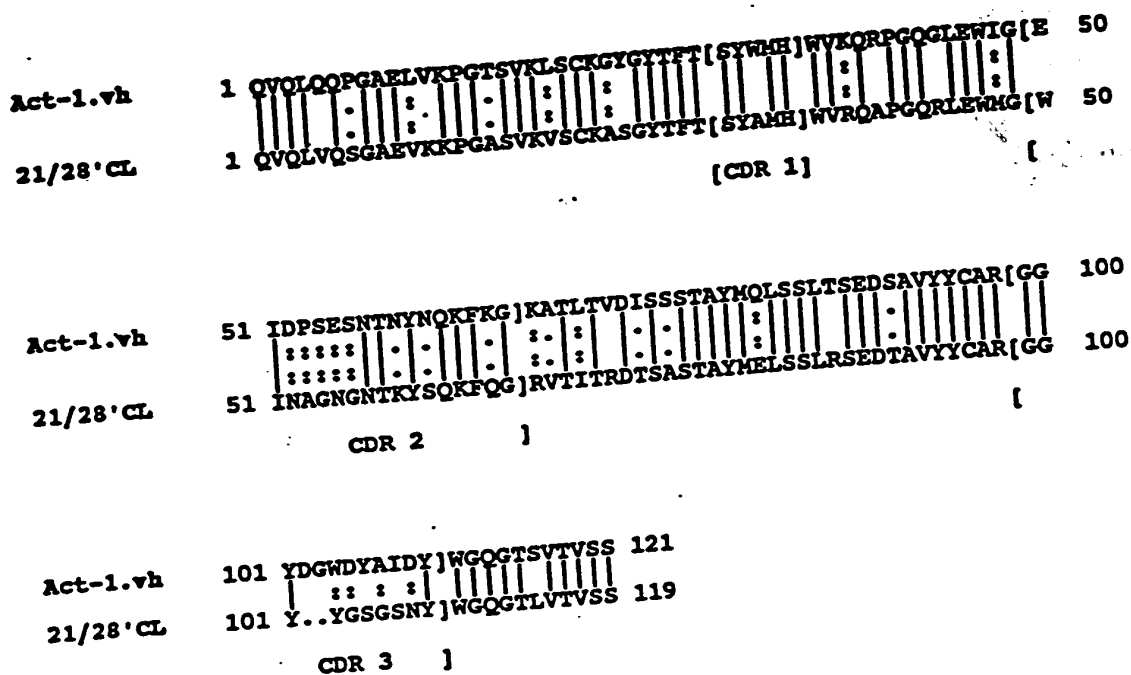
```
                                                                    50
Act-1.vh    1 QVQLQQPGAELVKPGTSVKLSCKGYGYTFT[SYWMH]WVKQRPGQGLEWIG[E  50
              |||||  | || ||||||| |  : ||||||  :  :  |||  | |  ||||| |
                                                                    50
21/28'CL    1 QVQLVQSGAEVKKPGASVKVSCKASGYTFT[SYAMH]WVRQAPGQRLEWMG[W  50
                                              [CDR 1]              [
```

```
                                                                    100
Act-1.vh   51 IDPSESNTNYNQKFKG]KATLTVDISSSTAYMQLSSLTSEDSAVYYCAR[GG  100
              :::::  | |  | |  : :  |  | |  | ||||| |||| | |||||| ||
                                                                    100
21/28'CL   51 INAGNGNTKYSQKFQG]RVTITRDTSASTAYMELSSLRSEDTAVYYCAR[GG  100
                  CDR 2       ]                                    [
```

```
Act-1.vh  101 YDGWDYAIDY]WGQGTSVTVSS 121
              |  :: : :|  ||||| |||||
21/28'CL  101 Y..YGSGSNY]WGQGTLVTVSS 119
                  CDR 3    ]
```

FIGURE 6

```
       ATGAAGTTGCCTGTTAGGCTGTTGGTGCTTCTGTTGTTCTGGATTCCTGTTTCCGGAGGT
1      ------+---------+---------+---------+---------+---------+ 60
       TACTTCAACGGACAATCCGACAACCACGAAGACAACAAGACCTAAGGACAAAGGCCTCCA
      [M  K  L  P  V  R  L  L  V  L  L  L  F  W  I  P  V  S  G  G]
                          Signal Peptide


       GATGTTGTGGTGACTCAAACTCCACTCTCCCTGCCTGTCAGCTTTGGAGATCAAGTTTCT
61     ------+---------+---------+---------+---------+---------+ 120
       CTACAACACCACTGAGTTTGAGGTGAGAGGGACGGACAGTCGAAACCTCTAGTTCAAAGA
      [D  V  V  V  T  Q  T  P  L  S  L  P  V  S  F  G  D  Q  V  S
                          Framework 1


       ATCTCTTGCAGGTCTAGTCAGAGTCTTGCAAAGAGTTATGGGAACACCTATTTGTCTTGG
121    ------+---------+---------+---------+---------+---------+ 180
       TAGAGAACGTCCAGATCAGTCTCAGAACGTTTCTCAATACCCTTGTGGATAAACAGAACC
       I  S  C][R  S  S  Q  S  L  A  K  S  Y  G  N  T  Y  L  S][W
                               CDR 1


       TACCTGCACAAGCCTGGCCAGTCTCCACAGCTCCTCATCTATGGGATTTCCAACAGATTT
181    ------+---------+---------+---------+---------+---------+ 240
       ATGGACGTGTTCGGACCGGTCAGAGGTGTCGAGGAGTAGATACCCTAAAGGTTGTCTAAA
       Y  L  H  K  P  G  Q  S  P  Q  L  L  I  Y][G  I  S  N  R  F
                          Framework 2                    CDR 2


       TCTGGGGTGCCAGACAGGTTCAGTGGCAGTGGTTCAGGGACAGATTTCACACTCAAGATC
241    ------+---------+---------+---------+---------+---------+ 300
       AGACCCCACGGTCTGTCCAAGTCACCGTCACCAAGTCCCTGTCTAAAGTGTGAGTTCTAG
       S][G  V  P  D  R  F  S  G  S  G  S  G  T  D  F  T  L  K  I
                          Framework 3


       AGCACAATAAAGCCTGAGGACTTGGGAATGTATTACTGCTTACAAGGTACACATCAGCCG
301    ------+---------+---------+---------+---------+---------+ 360
       TCGTGTTATTTCGGACTCCTGAACCCTTACATAATGACGAATGTTCCATGTGTAGTCGGC
       S  T  I  K  P  E  D  L  G  M  Y  Y  C][L  Q  G  T  H  Q  P
                                                         CDR3


            TACACGTTCGGAGGGGGGACCAAGCTGGAAATAAAA
361         ------+---------+---------+------ 396
            ATGTGCAAGCCTCCCCCCTGGTTCGACCTTTATTTT
            Y  T][F  G  G  G  T  K  L  E  I  K]
                          Framework 4
```

FIGURE 7

```
      GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCCGGCCTCC
    1 ------------+---------+---------+---------+---------+---------+ 60
      CTATAACACTACTGAGTCAGAGGTGAGAGGGACGGGCAGTGGGGACCTCTCGGCCGGAGG

      [D   I   V   M   T   Q   S   P   L   S   L   P   V   T   P   G   E   P   A   S
                                Framework 1
```

```
      ATCTCCTGCAGGTCTAGTCAGAGCCTCCTCCATAGTAATGGATCAAACTATTTGGATTGG
   61 ------------+---------+---------+---------+---------+---------+ 120
      TAGAGGACGTCCAGATCAGTCTCGGAGGAGGTATCATTACCTAGTTTGATAAACCTAACC

       I   S   C][R   S   S   Q   S   L   L   H   S   N   G   Y   N   Y   L   D][W
                                CDR 1
```

```
      TACCTGCAGAAGCCAGGGCAGTCTCCACAGCTCCTGATCTATTTGGGTTCTAATCGGGCC
  121 ------------+---------+---------+---------+---------+---------+ 180
      ATGGACGTCTTCGGTCCCGTCAGAGGTGTCGAGGACTAGATAAACCCAAGATTAGCCCGG

       Y   L   Q   K   P   G   Q   S   P   Q   L   L   I   Y][L   G   S   N   R   A
                      Framework 2                              CDR 2
```

```
      TCCGGGGTCCCTGACAGGTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAATC
  181 ------------+---------+---------+---------+---------+---------+ 240
      AGGCCCCAGGGACTGTCCAAGTCACCGTCACCTAGTCCGTGTCTAAAATGTGTCTTTTAG

       S][G   V   P   D   R   F   S   G   S   G   S   G   T   D   F   T   L   K   I
                                Framework 3
```

```
      AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGCATGCAAGCTCTACCAACTCCT
  241 ------------+---------+---------+---------+---------+---------+ 300
      TCGTCTCACCTCCGACTCCTACAACCCCAAATAATGACGTACGTTCGAGATGGTTGAGGA

       S   R   V   E   A   E   D   V   G   V   Y   Y   C][M   Q   A   L   Q   T   P
                                                          CDR 3
```

```
      CAGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA
  301 ------------+---------+---------+------ 336
      GTCTGCAAGCCGGTTCCCTGGTTCCACCTTTAGTTT

       Q   T][F   G   Q   G   T   K   V   E   I   K]
                      Framework 4
```

FIGURE 8

ATGGGATGGAGCTGTATCATCCTCTTCTTGGTATCAACAGCTACAAGTGTCCACTCCCAG
1 ----------+---------+---------+---------+---------+---------+ 60
TACCCTACCTCGACATAGTAGGAGAAGAACCATAGTTGTCGATGTTCACAGGTGAGGGTC

M G W S C I I L F L V S T A T S V H S][Q

Signal Peptide

GTCCAACTGCAGCAGCCTGGGGCTGAGCTTGTGAAGCCTGGGACTTCAGTGAAGCTGTCC
61 ----------+---------+---------+---------+---------+---------+ 120
CAGGTTGACGTCGTCGGACCCCGACTCGAACACTTCGGACCCTGAAGTCACTTCGACAGG

V Q L Q Q P G A E L V K P G T S V K L S

Framework 1

TGCAAGGGTTATGGCTACACCTTCACCAGCTACTGGATGCACTGGGTGAAGCAGAGGCCT
121 ----------+---------+---------+---------+---------+---------+ 180
ACGTTCCCAATACCGATGTGGAAGTGGTCGATGACCTACGTGACCCACTTCGTCTCCGGA

C K G Y G Y T F T][S Y W M H][W V K Q R P

CDR 1

GGACAAGGCCTTGAGTGGATCGGAGAGATTGATCCTTCTGAGAGTAATACTAACTACAAT
181 ----------+---------+---------+---------+---------+---------+ 240
CCTGTTCCGGAACTCACCTAGCCTCTCTAACTAGGAAGACTCTCATTATGATTGATGTTA

G Q G L E W I G][E I D P S E S N T N Y N

Framework 2   CDR 2

CAAAAATTCAAGGGCAAGGCCACATTGACTGTAGACATTTCCTCCAGCACAGCCTACATG
241 ----------+---------+---------+---------+---------+---------+ 300
GTTTTTAAGTTCCCGTTCCGGTGTAACTGACATCTGTAAAGGAGGTCGTGTCGGATGTAC

Q K F K G][K A T L T V D I S S S T A Y M

Framework 3

CAGCTCAGCAGCCTGACATCTGAGGACTCTGCGGTCTACTATTGTGCAAGAGGGGGGTTAC
301 ----------+---------+---------+---------+---------+---------+ 360
GTCGAGTCGTCGGACTGTAGACTCCTGAGACGCCAGATGATAACACGTTCTCCCCCAATG

Q L S S L T S E D S A V Y Y C A R][G G Y

GACGGATGGGACTATGCTATTGACTACTGGGGTCAAGGCACCTCAGTCACCGTCTCCTCA
361 ----------+---------+---------+---------+---------+---------+ 420
CTGCCTACCCTGATACGATAACTGATGACCCCAGTTCCGTGGAGTCAGTGGCAGAGGAGT

D G W D Y A I D Y][W G Q G T S V T V S S]

CDR 3   Framework 4

FIGURE 9

ATGGAGTTTGGGCTGAGCTGGCTTTTTCTTGTGGCTATTTTAAAAGGTGTCCAGTGTCAG
1 ---------+---------+---------+---------+---------+---------+ 60
TACCTCAAACCCGACTCGACCGAAAAAGAACACCGATAAAATTTTCCACAGGTCACAGTC

[M E F G L S W L F L V A I L K G V Q C][Q
Signal peptide

GTGCAGCTTGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCC
61 ---------+---------+---------+---------+---------+---------+ 120
CACGTCGAACACGTCAGACCCCGACTCCACTTCTTCGGACCCCGGAGTCACTTCCAAAGG

V Q L V Q S G A E V K K P G A S V K V S
Framework 1

TGCAAGGCTTCTGGATACACCTTCACTAGCTATGCTATGCATTGGGTGCGCCAGGCCCCC
121 ---------+---------+---------+---------+---------+---------+ 180
ACGTTCCGAAGACCTATGTGGAAGTGATCGATACGATACGTAACCCACGCGGTCCGGGGG

C K A S G Y T F T][S Y A M H][W V R Q A P
CDR 1

GGACAAAGGCTTGAGTGGATGGGATGGATCAACGCTGGCAATGGTAACACAAAATATTCA
181 ---------+---------+---------+---------+---------+---------+ 240
CCTGTTTCCGAACTCACCTACCCTACCTAGTTGCGACCGTTACCATTGTGTTTTATAAGT

G Q R L E W M G][W I N A G N G N T K Y S
Framework 2   CDR 2

CAGAAGTTCCAGGGCAGAGTCACCATTACCAGGGACACATCCGCGAGCACAGCCTACATG
241 ---------+---------+---------+---------+---------+---------+ 300
GTCTTCAAGGTCCCGTCTCAGTGGTAATGGTCCCTGTGTAGGCGCTCGTGTCGGATGTAC

Q K F Q G][R V T I T R D T S A S T A Y M

GAGCTGAGCAGCCTGAGATCTGAAGACACGGCTGTGTATTACTGTGCGAGAGGAGGTTAC
301 ---------+---------+---------+---------+---------+---------+ 360
CTCGACTCGTCGGACTCTAGACTTCTGTGCCGACACATAATGACACGCTCTCCTCCAATG

E L S S L R S E D T A V Y Y C A R][G G Y
Framework 3

TATGGTTCGGGGAGCAACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
361 ---------+---------+---------+---------+---------+---- 414
ATACCAAGCCCCTCGTTGATGACCCCGGTCCCTTGGGACCAGTGGCAGAGGAGT

Y G S G S N Y][W G Q G T L V T V S S]
CDR 3   Framework 4

FIGURE 10

Sequence Range: 1 to 540

```
              10          20          30          40
      *        *    *      *    *      *    *      *     *
ATG AAA TGC ACC TGG GTC ATT CTC TTC TTG GTA TCA ACA GCT ACA AGT
 M   K   C   T   W   V   I   L   F   L   V   S   T   A   T   S>
                Signal peptide cleavage site
                                 SpeI
 50         60          70          80          90
  *          *    *      *    *      *    *      *    *
GTC CAC TCC CAG GTC CAA CTA GTG CAG TCT GGG GCT GAG GTT AAG AAG
 V   H   S   Q   V   Q   L   V   Q   S   G   A   E   V   K   K>

   100         110         120         130         140
    *     *      *    *      *    *      *    *      *    *
CCT GGG GCT TCA GTG AAG GTG TCC TGC AAG GGT TCT GGC TAC ACC TTC
 P   G   A   S   V   K   V   S   C   K   G   S   G   Y   T   F>
                                                          190
        150         160         170         180
   *      *    *      *    *      *    *      *    *
ACC AGC TAC TGG ATG CAT TGG GTG AGG CAG GCG CCT GGC CAA CGT CTA
 T   S   Y   W   M   H   W   V   R   Q   A   P   G   Q   R   L>

         200         210         220         230         240
    *      *    *      *    *      *    *      *    *      *
GAG TGG ATC GGA GAG ATT GAT CCT TCT GAG AGT AAT ACT AAC TAC AAT
 E   W   I   G   E   I   D   P   S   E   S   N   T   N   Y   N>
                                                          NheI
           250         260         270         280
      *      *    *      *    *      *    *      *    *
CAA AAA TTC AAG GGA CGC GTC ACA TTG ACT GTA GAC ATT TCC GCT AGC
 Q   K   F   K   G   R   V   T   L   T   V   D   I   S   A   S>

290         300         310         320         330
 *           *    *      *    *      *    *      *    *
ACA GCC TAC ATG GAG CTC AGC AGC CTG AGA TCT GAG GAC ACT GCG GTC
 T   A   Y   M   E   L   S   S   L   R   S   E   D   T   A   V>

        340         350         360         370         380
   *      *    *      *    *      *    *      *    *      *
TAC TAT TGT GCA AGA GGG GGT TAC GAC GGA TGG GAC TAT GCT ATT GAC
 Y   Y   C   A   R   G   G   Y   D   G   W   D   Y   A   I   D>
                                  BstBI                 Constant region
         390         400         410         420         430
    *      *    *      *    *      *    *      *    *      *
TAC TGG GGT CAA GGC ACC CTG GTC ACG GTC TCC TCA GCC TCC ACC AAG
 Y   W   G   Q   G   T   L   V   T   V   S   S   A   S   T   K>

            440         450         460         470         480
       *      *    *      *    *      *    *      *    *      *
GGC CCA TCG GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG
 G   P   S   V   F   P   L   A   P   S   S   K   S   T   S   G>
                                                          AgeI
            490         500         510         520
       *      *    *      *    *      *    *      *
GGC ACA GCG GCC CTG GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG
 G   T   A   A   L   G   C   L   V   K   D   Y   F   P   E   P>

 530         540
  *           *
GTG ACG GTG TCG
 V   T   V   S>
```

FIGURE 11

Sequence Range: 1 to 413

```
              10              20              30              40
              *               *               *               *
    *         *       *        *       *       *       *       *
ATG AAG TTG CCT GTT AGG CTG TTG GTG CTT CTG TTG TTC TGG ATT CCT
 M   K   L   P   V   R   L   L   V   L   L   L   F   W   I   P>
```

Signal peptide cleavage site

```
50   BsaEI   60              70              80              90
 *    *       *       *       *       *       *       *       *
GTT TCC GGA GGT GAT GTT GTG ATG ACT CAA AGT CCA CTC TCC CTG CCT
 V   S   G   G   D   V   V   M   T   Q   S   P   L   S   L   P>
```

```
    100             110             120         130         140
     *               *               *           *           *
     *       *       *       *       *       *       *       *
GTC ACC CCT GGA GAA CCA GCT TCT ATC TCT TGC AGG TCT AGT CAG AGT
 V   T   P   G   E   P   A   S   I   S   C   R   S   S   Q   S>
```

```
       150             160             170      180 Asp718  190
        *       *        *       *       *        *          *
  *     *       *        *       *       *        *          *
CTT GCA AAG AGT TAT GGG AAC ACC TAT TTG TCT TGG TAC CTG CAG AAG
 L   A   K   S   Y   G   N   T   Y   L   S   W   Y   L   Q   K>
```

```
          200             210             220      230      240
           *       *        *       *       *        *        *
    *      *       *        *       *       *        *        *
CCT GGC CAG TCT CCA CAG CTC CTC ATC TAT GGG ATT TCC AAC AGA TTT
 P   G   Q   S   P   Q   L   L   I   Y   G   I   S   N   R   F>
```

```
       250             260             270         280
        *       *        *       *       *           *       *
  *     *       *        *       *       *           *       *
TCT GGG GTG CCA GAC AGG TTC AGT GGC AGT GGT TCA GGG ACA GAT TTC
 S   G   V   P   D   R   F   S   G   S   G   S   G   T   D   F>
```

```
290             300    NruI    310             320         330
 *       *       *        *       *       *       *           *
 *       *       *        *       *       *       *           *
ACA CTC AAG ATC TCG CGA GTA GAG GCT GAG GAC GTG GGA GTG TAT TAC
 T   L   K   I   S   R   V   E   A   E   D   V   G   V   Y   Y>
```

```
   340             350             360         370         380
    *       *        *       *       *           *           *
    *       *        *       *       *           *           *
TGC TTA CAA GGT ACA CAT CAG CCG TAC ACG TTC GGA CAG GGG ACC AAG
 C   L   Q   G   T   H   Q   P   Y   T   F   G   Q   G   T   K>
```

```
    390             400             410 KasI
     *       *        *       *       *
     *       *        *       *       *
GTG GAA ATA AAA CGG GCT GAT GCG GCG CC
 V   E   I   K   R   A   D   A   A   P>
```

FIGURE 12

LIGHT CHAIN OLIGOS:

L1 5'- TTT CCG GAG GTG ATG TTG TGA TGA CTC AAA GTC CAC TCT CCC
TGC CTG TCA CCC CTG GAG AAC CAG CTT CTA TCT CTT GCA
GGT CTA GTC AGA G

LA

L2 5'- ACT GGC CAG GCT TCT GCA GGT ACC AAG ACA AAT AGG TGT TCC
CAT AAC TCT TTG CAA GAC TCT GAC TAG ACC TGC AAG AGA
TAG AAG CTG GTT C

L3 5'- CCT GGC CAG TCT CCA CAG CTC CTC ATC TAT GGG ATT TCC AAC
AGA TTT TCT GGG GTG CCA GAC AGG TTC AGT GGC AGT GGT
TC

LB

L4 5'- ACT CGC GAG ATC TTG AGT GTG AAA TCT GTC CCT GAA CCA CTG
CCA CTG AAC CTG TCT GGC ACC CCA GAA AAT CTG TTG GAA
ATC

L5 5'- TCT CGC GAG TAG AGG CTG AGG ACG TGG GAG TGT ATT ACT GCT
TAC AAG GTA CAC ATC AGC CGT ACA C

LC

L6 5'- ATG GCG CCG CAT CAG CCC GTT TTA TTT CCA CCT TGG TCC CCT
GTC CGA ACG TGT ACG GCT GAT GTG TAC CTT GTA AGC AGT
AAT AC

HEAVY CHAIN OLIGOS

H1 5'- ATA AGC TTC GCC ATG AAA TGC ACC TGG GTC ATT CTC TTC TTG
GTA TCA ACA GCT ACA AGT GTC CAC TCC CAG GTC CAA CTA
GTG CAC CGG TTA

HA

H2 5'- TAA CCG GTG CAC TAG TTG GAC CTG GGA GTG GAC ACT TGT AGC
TGT TGA TAC CAA GAA GAG AAT GAC CCA GGT GCA TTT CAT
GGC GAA GCT TAT

H3 5'- CAA CTA GTG CAG TCT GGG GCT GAG GTT AAG AAG CCT GGG GCT
TCA GTG AAG GTG TCC TGC AAG GGT TCT GGC TAC ACC TTC
ACC AGC

HB

H4 5'- TAA CCG GTA CTC TAG ACG TTG GCC AGG CGC CTG CCT CAC CCA
ATG CAT CCA GTA GCT GGT GAA GGT GTA GCC AGA ACC CTT
GCA GGA C

H5 5'- CGT CTA GAG TGG ATC GGA GAG ATT GAT CCT TCT GAG AGT AAT
ACT AAC TAC AAT CAA AAA TTC AAG GGA CGC GTC A

HC

H6 5'- TAA CCG GTG TGC TAG CGG AAA TGT CTA CAG TCA ATG TGA CGC
GTC CCT TGA ATT TTT GAT TGT AGT TAG TAT TAC T

H7 5'- CCG CTA GCA CAG CCT ACA TGG AGC TCA GCA GCC TGA GAT CTG
AGG ACA CTG CGG TCT ACT ATT GTG CAA GAG GGG GTT ACG
ACG GAT G

HD

H8 5'- TCA CCG GTG CGG TGA CCA GGG TGC CTT GAC CCC AGT AGT CAA
TAG CAT AGT CCC ATC CGT CGT AAC CCC CTC TTG CAC AAT
AGT AGA C

H9 5'- CTG GTC ACC GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG GTC
TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG GGC
ACA G

HE

H10 5'- TCA CCG GTT CGG GGA AGT AGT CCT TGA CCA GGC AGC CCA
GGG CCG CTG TGC CCC CAG AGG TGC TCT TGG AGG AGG GTG
CCA GGG G

FIGURE 13

FIGURE 14

TITRATION
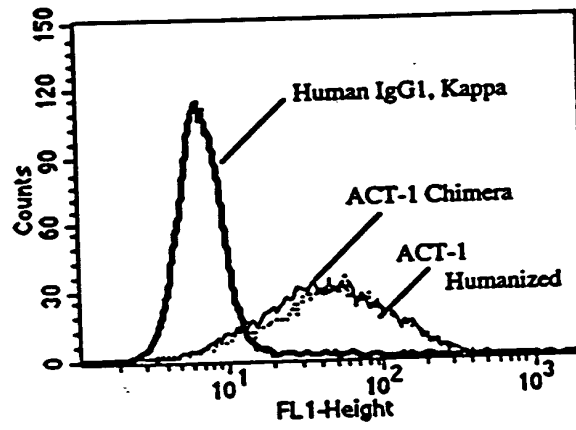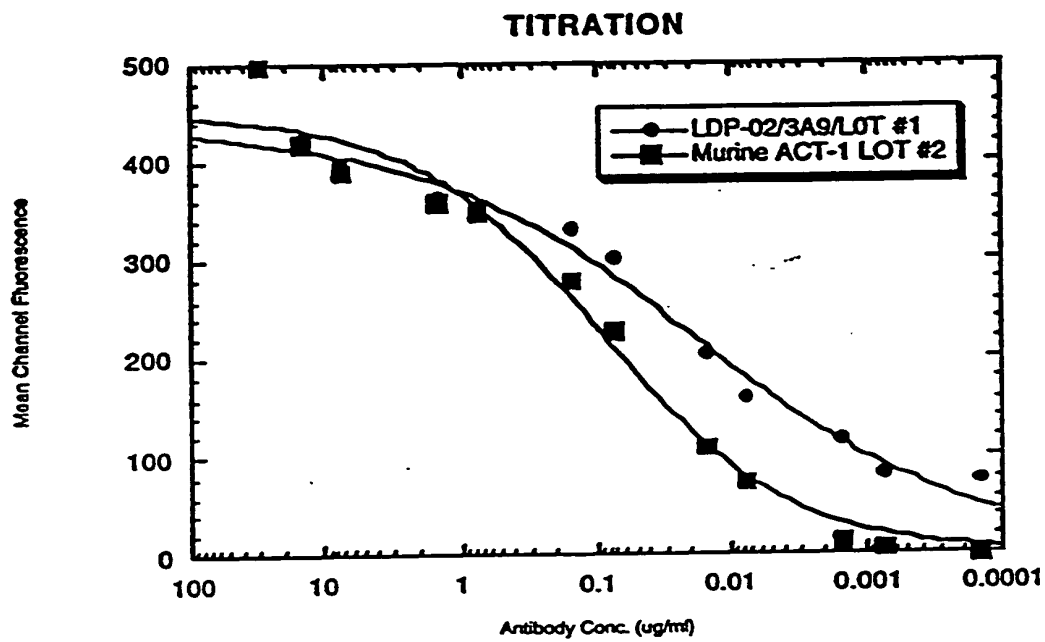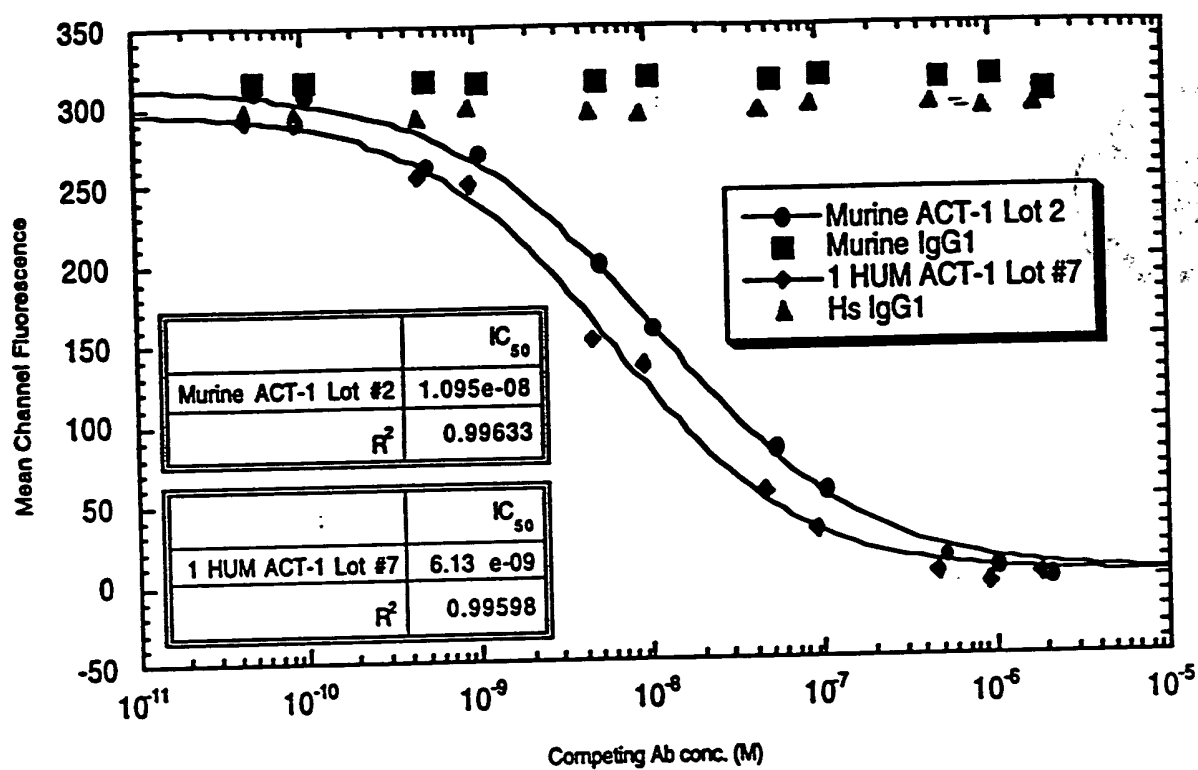

FIGURE 15

FIGURE 16

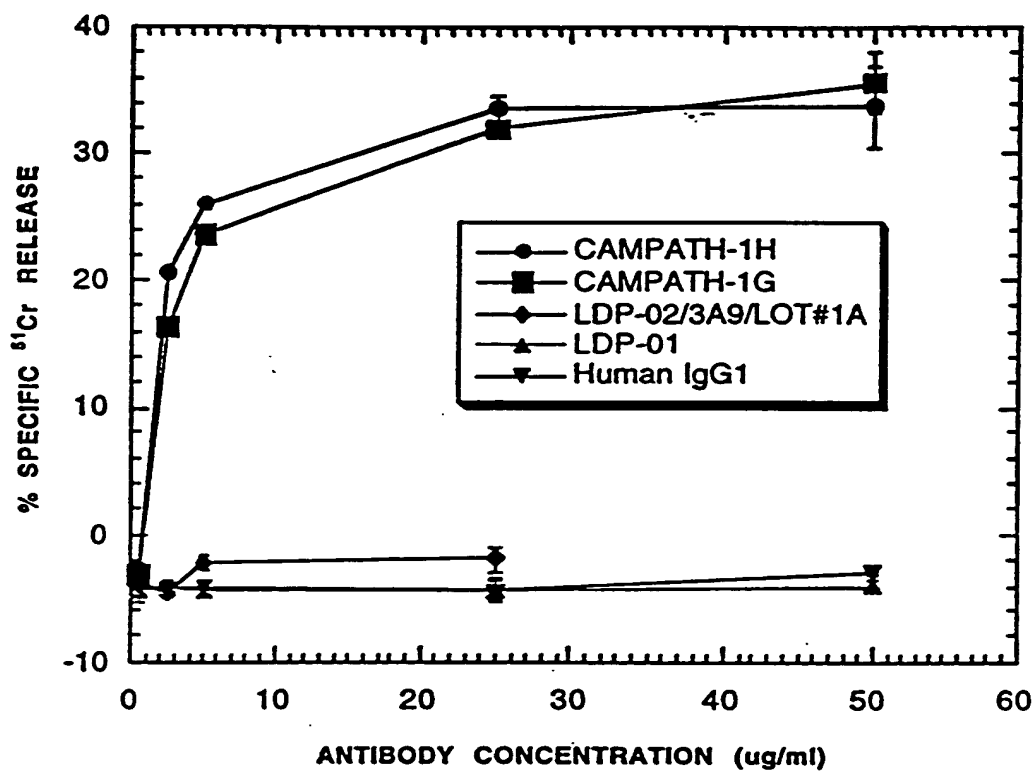## LDP-02 DOES NOT PARTICIPATE IN COMPLEMENT MEDIATED CELL LYSIS

FIGURE 17
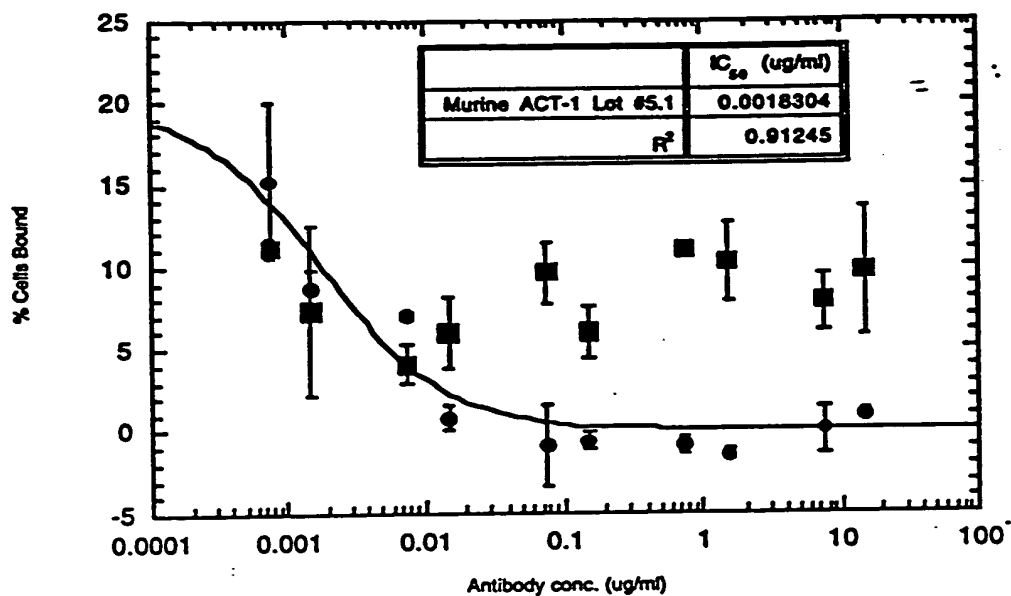
ADHESION ASSAY

FIGURE 18A

ADHESION ASSAY

FIGURE 18B

FIGURE 19